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EXAMINER
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STEADMAN, DAVID J

ART UNIT	PAPER NUMBER
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1656

DATE MAILED: 10/20/2006

Please find below and/or attached an Office communication concerning this application or proceeding.

**Office Action Summary**

Application No.

10/720,460

Applicant(s)

OHNO, SHIGEO

Examiner

David J. Steadman

Art Unit

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-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

**Period for Reply**

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

**Status**

- 1) ☒ Responsive to communication(s) filed on 05 December 2005 and 03 August 2006.
- 2a) ☐ This action is **FINAL**. 2b) ☒ This action is non-final.
- 3) ☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

**Disposition of Claims**

- 4) ☒ Claim(s) 1-14 and 16-20 is/are pending in the application.
- 4a) Of the above claim(s) 4-14, 18 and 19 is/are withdrawn from consideration.
- 5) ☐ Claim(s) \_\_\_\_\_ is/are allowed.
- 6) ☒ Claim(s) 1-3, 16, 17 and 20 is/are rejected.
- 7) ☐ Claim(s) \_\_\_\_\_ is/are objected to.
- 8) ☐ Claim(s) \_\_\_\_\_ are subject to restriction and/or election requirement.

**Application Papers**

- 9) ☒ The specification is objected to by the Examiner.
- 10) ☐ The drawing(s) filed on \_\_\_\_\_ is/are: a) ☐ accepted or b) ☐ objected to by the Examiner.  
Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).  
Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).
- 11) ☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

**Priority under 35 U.S.C. § 119**

- 12) ☒ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).
- a) ☒ All b) ☐ Some \* c) ☐ None of:
1. ☐ Certified copies of the priority documents have been received.
  2. ☐ Certified copies of the priority documents have been received in Application No. \_\_\_\_\_.
  3. ☒ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

\* See the attached detailed Office action for a list of the certified copies not received.

**Attachment(s)**

- |  |   |
|--|---|
| 1) <input checked="" type="checkbox"/> Notice of References Cited (PTO-892)  | 4) <input type="checkbox"/> Interview Summary (PTO-413)<br>Paper No(s)/Mail Date. _____ |
| 2) <input type="checkbox"/> Notice of Draftsperson's Patent Drawing Review (PTO-948)   | 5) <input type="checkbox"/> Notice of Informal Patent Application                       |
| 3) <input checked="" type="checkbox"/> Information Disclosure Statement(s) (PTO/SB/08)<br>Paper No(s)/Mail Date <u>8/9/04, 8/3/06.</u> | 6) <input checked="" type="checkbox"/> Other: <u>Appendices A, B, C.</u>                |

## **DETAILED ACTION**

### ***Status of the Application***

**[1]** The Art Unit location of your application in the USPTO has changed. To aid in correlating any papers for this application, all further correspondence regarding this application should be directed to Art Unit 1656.

**[2]** Claims 1-14 and 16-20 are pending in the application.

**[3]** Applicant's amendment to the claims, filed 5 December 2005 is acknowledged. This listing of the claims replaces all prior versions and listings of the claims.

**[4]** Receipt of an information disclosure statement, filed 3 August 2006, in response to a request for information under 37 CFR 1.105, mailed 17 February 2006, is acknowledged.

### ***Election/Restriction***

**[5]** Applicant's election without traverse of Group I, claims 1-3 and 16-17, in the reply filed on 12/5/2005, is acknowledged.

**[6]** Claims 4-14 and 18-19 are withdrawn from further consideration pursuant to 37 CFR 1.142(b) as being drawn to nonelected inventions, there being no allowable generic or linking claim.

**[7]** Claims 1-3, 16-17, and newly added claim 20, which depends from claim 16, are being examined on the merits. Claims 16-17 have been examined only to the extent the claims read on the elected subject matter.

***Claim to Domestic and Foreign Priority***

**[8]** Applicants' claim to domestic priority under 35 U.S.C. § 120 to PCT/JP01/10234, filed 22 November 2001, is acknowledged. Applicant's claim to foreign priority under 35 U.S.C. § 119(a)-(d) to Japanese application JP 2001-156088, having the priority date of 24 May 2001, is acknowledged. A certified copy of the foreign priority document has been filed in the instant application.

***Information Disclosure Statement***

**[9]** With the exception of reference CC of the IDS filed 9 August 2004, all references cited in the IDSs filed 9 August 2004 and 3 August 2006 have been considered by the examiner. A copy of Forms PTO-1449 is attached to the instant Office action. Reference CC of the IDS filed 9 August 2004 is lined through as this citation is a duplicate of reference CC of the IDS filed 3 August 2006.

***Specification/Informalities***

**[10]** The title of the invention is not descriptive. A new title is required that is clearly indicative of the invention to which the claims are directed. The following title is suggested: --Human SMG-1 Polypeptide--.

***Claim Objection(s)***

**[11]** Claims 1 and 16 are objected to in the recitation of "SMG-1." Abbreviations, unless otherwise obvious and/or commonly used in the art, should not be recited in the

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claims without at least once reciting the entire phrase for which the abbreviation is used.

Appropriate correction is required.

**[12]** Claim 1 is objected to as using a confusing format. The claim lists parts (1) and (2) and it is unclear as to whether applicant intends for parts (1) and (2) to be jointly included in claim 1 or whether parts (1) and (2) are intended as being separate claims. Appropriate correction is required.

***Claim Rejections - 35 USC § 112, Second Paragraph***

The following is a quotation of the second paragraph of 35 U.S.C. 112:

The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

**[13]** Claim(s) 16 and 20 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

The term "SMG-1 mutant" in claim 16 (claim 20 dependent therefrom) is a relative term which renders the claim indefinite as there is no indication in the claims or the specification as the sequence(s) of an SMG-1 polypeptide or polypeptides that applicant considers to be "non-mutant" and/or "mutant" such that a skilled artisan would have a reference sequence or sequences in order to make a determination of those polypeptides that are considered to be "mutant" SMG-1 polypeptides and those that are considered to be "non-mutant." As such, it is unclear as to the scope of SMG-1 polypeptides that are encompassed by the claim. In the interest of advancing

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prosecution, the examiner has interpreted the term as encompassing any polypeptide variants of SEQ ID NO:2, including those that maintain SMG-1 activity.

***Claim Rejections - 35 USC § 101***

35 U.S.C. 101 reads as follows:

Whoever invents or discovers any new and useful process, machine, manufacture, or composition of matter, or any new and useful improvement thereof, may obtain a patent therefor, subject to the conditions and requirements of this title.

**[14]** Claims 1-3 and 16-17 are rejected under 35 U.S.C. 101 because the claimed invention is directed to non-statutory subject matter. The claims are drawn to polypeptides or agents. The claims read on a product of nature and should be amended to indicate the hand of the inventor, e.g., by insertion of "purified" or "isolated". See MPEP § 2105.

***Claim Rejections - 35 USC § 112, First Paragraph***

The following is a quotation of the first paragraph of 35 U.S.C. 112:

The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

**[15]** Claims 16 and 20 are rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the written description requirement. The claim(s) contain subject matter which was not described in the specification in such a way as to reasonably convey to

one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention. This is a new matter rejection.

MPEP § 2163 states, "when filing an amendment an applicant should show support in the original disclosure for new or amended claims" (MPEP 8<sup>th</sup> Ed., October 2006 Revision at pp. 2100-176 and 2100-183) and "[i]f the originally filed disclosure does not provide support for each claim limitation, or if an element which applicant describes as essential or critical is not claimed, a new or amended claim must be rejected under 35 U.S.C. 112, para. 1, as lacking adequate written description."

Claim 16 (claim 20 dependent therefrom) has been amended on 5 December 2005 to delete the term "activity-deficient," thus broadening the scope of claimed agents for suppressing nonsense-mediated mRNA decay to comprising any SMG-1 mutant. In the response accompanying the amendment, applicant fails to show support for the amendment to claim 16. While the examiner can find support for an agent for suppressing nonsense-mediated mRNA decay comprising an *activity-deficient* SMG-1 mutant, the examiner can find no support for an agent for suppressing nonsense-mediated mRNA decay to comprising *any* SMG-1 mutant. Applicant is invited to show support for the claim limitation at issue.

**[16]** Claims 1-2, 16-17, and 20 are rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the written description requirement. The claim(s) contain subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application

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was filed, had possession of the claimed invention. This is a written description rejection.

Claim 1 (claim 17 dependent therefrom) is drawn to (in relevant part) a genus of polypeptides having SMG-1 activity and comprising any variant of amino acids 129 to 3657 of SEQ ID NO:2. Claim 2 is drawn to (in relevant part) a genus of polypeptides having SMG-1 activity and comprising a polypeptide having at least 90% homology (interpreted as meaning identity) to amino acids 129-3657 of SEQ ID NO:2, amino acids 1-3657 of SEQ ID NO:2, or amino acids 107-3657 of SEQ ID NO:2. The specification defines "SMG-1 activity" as "an activity of phosphorylating Upf1/SMG-2 [Sun, X. et al., Proc. Natl. Acad. Sci. USA, 95, 10009-10014 (1998); and Bhattacharya, A. et al., RNA, 6, 1226-1235 (2000)]" (specification at p. 6, lines 17-20). Claims 16 and 20 are drawn to (in relevant part) an agent for suppressing nonsense-mediated mRNA decay comprising a genus of SMG-1 mutants having any structure and any activity and optionally further comprising any aminoglycoside antibiotic having any structure ["aminoglycoside antibiotic" is defined in the specification as being "not particularly limited, so long as it has a nonsense suppression activity alone," specification at p. 34, 2<sup>nd</sup> full paragraph].

The Court of Appeals for the Federal Circuit has held that a "written description of an invention involving a chemical genus, like a description of a chemical species, 'requires a precise definition, such as by structure, formula [or] chemical name,' of the claimed subject matter sufficient to distinguish it from other materials." For claims drawn to a genus, MPEP § 2163 states the written description requirement for a claimed genus may be satisfied through sufficient description of a representative number of species by



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actual reduction to practice, reduction to drawings, or by disclosure of relevant, identifying characteristics, i.e., structure or other physical and/or chemical properties, by functional characteristics coupled with a known or disclosed correlation between function and structure, or by a combination of such identifying characteristics, sufficient to show the applicant was in possession of the claimed genus. MPEP § 2163 states that a representative number of species means that the species which are adequately described are representative of the entire genus. Thus, when there is substantial variation within the genus, one must describe a sufficient variety of species to reflect the variation within the genus. In this case, the specification discloses only a single species of the genus of polypeptides of claims 1-2, i.e., SEQ ID NO:2, and only a single species of the genus of recited polypeptides of claim 16, i.e., SEQ ID NO:2 with a single mutation, wherein the mutation is Asp at position 2331 replaced with Ala [specification at p. 34, 3<sup>rd</sup> full paragraph]. Other than this single representative species, the specification fails to disclose any other additional representative species of the genus of claimed polypeptides. While MPEP § 2163 acknowledges that in certain situations “one species adequately supports a genus,” it is also acknowledges that “[f]or inventions in an unpredictable art, adequate written description of a genus which embraces widely variant species cannot be achieved by disclosing only one species within the genus.” In the instant case, the claimed genus of polypeptides of claims 1-2 encompasses species that are widely variant with respect to structure [because the genus of polypeptides is limited to those having “SMG-1 activity” as defined above, the genus is not considered to have widely variant functions] and the genus of polypeptides of claim 16

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encompasses species that are widely variant with respect to structure *and* function. As such, the disclosure of the single representative species of polypeptides of claims 1-2, *i.e.*, SEQ ID NO:2 or single representative species of polypeptides of claim 16, *i.e.*, SEQ ID NO:2 with a single mutation, wherein the mutation is an Asp to Ala mutation at position 2331, is insufficient to be representative of the attributes and features of all species encompassed by the claimed genus of claimed or recited polypeptides.

Given the lack of description of a representative number of polynucleotides, the specification fails to sufficiently describe the claimed invention in such full, clear, concise, and exact terms that a skilled artisan would recognize that applicant was in possession of the claimed invention.

**[17]** Claims 1-2, 16-17, and 20 are rejected under 35 U.S.C. 112, first paragraph, because the specification, while being enabling for the polypeptide of SEQ ID NO:2, does not reasonably provide enablement for all variants of SEQ ID NO:2, including SEQ ID NO:2 with a single mutation, wherein the mutation is an Asp to Ala mutation at position 2331, broadly encompassed by the claims. The specification does not enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and/or use the invention commensurate in scope with these claims.

It is the examiner's position that undue experimentation is required for a skilled artisan to make and/or use the entire scope of the claimed invention. Factors to be considered in determining whether undue experimentation is required are summarized in *In re Wands* (858 F.2d 731, 737, 8 USPQ2d 1400, 1404 (Fed. Cir. 1988)) as follows:

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(A) The breadth of the claims; (B) The nature of the invention; (C) The state of the prior art; (D) The level of one of ordinary skill; (E) The level of predictability in the art; (F) The amount of direction provided by the inventor; (G) The existence of working examples; and (H) The quantity of experimentation needed to make or use the invention based on the content of the disclosure. See MPEP § 2164.01(a). MPEP 2164.04 states, "[w]hile the analysis and conclusion of a lack of enablement are based on the factors discussed in MPEP § 2164.01(a) and the evidence as a whole, it is not necessary to discuss each factor in the written enablement rejection" and that "[t]he language should focus on those factors, reasons, and evidence that lead the examiner to conclude that the specification fails to teach how to make and use the claimed invention without undue experimentation, or that the scope of any enablement provided to one skilled in the art is not commensurate with the scope of protection sought by the claims." Accordingly, the Factors most relevant to the instant rejection are addressed in detail below.

*The breadth of the claims:* Claim 1 (claim 17 dependent therefrom) is drawn to (in relevant part) all polypeptides having SMG-1 activity and comprising any variant of SEQ ID NO:2. Claim 2 is drawn to (in relevant part) all polypeptides having SMG-1 activity and comprising a polypeptide having at least 90% homology (interpreted as meaning identity) to amino acids 129-3657 of SEQ ID NO:2, amino acids 1-3657 of SEQ ID NO:2, or amino acids 107-3657 of SEQ ID NO:2. It is noted that the specification defines "SMG-1 activity" as "an activity of phosphorylating Upf1/SMG-2 [Sun, X. et al., Proc. Natl. Acad. Sci. USA, 95, 10009-10014 (1998); and Bhattacharya, A. et al., RNA, 6, 1226-1235 (2000)]" (specification at p. 6, lines 17-20). Claims 16 and 20 are drawn to

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(in relevant part) an agent for suppressing nonsense-mediated mRNA decay comprising any SMG-1 mutant having any sequence of amino acids and any activity and optionally further comprising any aminoglycoside antibiotic having any structure ["aminoglycoside antibiotic which may be used in the pharmaceutical composition of the present invention for suppressing nonsense is not particularly limited, so long as it has a nonsense suppression activity alone," specification at p. 34, 2<sup>nd</sup> full paragraph]. The enablement provided by the specification is not commensurate in scope with the claims with regard to broad scope of polypeptides encompassed by the claims. In this case, the specification is enabling only for the polypeptide of SEQ ID NO:2.

*The state of the prior art; The level of one of ordinary skill; and The level of predictability*

*in the art:* The amino acid sequence of a polypeptide determines the polypeptide's structural and functional properties. Predictability of which changes can be tolerated in a protein's amino acid sequence and obtain the desired activity/utility requires a knowledge of and guidance with regard to which amino acids in the protein's sequence, if any, are tolerant of modification and which are conserved (*i.e.*, expectedly intolerant to modification), and detailed knowledge of the ways in which the proteins' structure relates to its function. The positions within a protein's sequence where modifications can be made with a reasonable expectation of success in obtaining a polypeptide having the desired activity/utility are limited in any protein and the result of such modifications is highly unpredictable. In addition, one skilled in the art would expect any tolerance to modification for a given protein to diminish with each further and additional modification, *e.g.*, multiple substitutions. At the time of the invention, methods for isolating or

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generating variants of a given polypeptide acid were known in the art. However, neither the specification nor the state of the art at the time of the invention provide the necessary guidance for altering the polypeptide of SEQ ID NO:2 with an expectation of obtaining a polypeptide having the desired activity/utility. At the time of the invention, there was a high level of unpredictability associated with altering a polypeptide sequence with an expectation that the polypeptide will maintain the desired activity/utility. For example, in the "Introduction to Protein Structure," [Branden and Tooze, Garland Publishing Inc., New York], it is disclosed that "[p]rotein engineers frequently have been surprised by the range of effects caused by single mutations that they hoped would change only one specific and simple property in enzymes" and "[t]he often surprising results of such experiments reveal how little we know about the rules of protein stability... ..they also serve to emphasize how difficult it is to design *de novo* stable proteins with specific functions" (page 247). The cited teachings of "Introduction to Protein Structure" are exemplified by the reference of Witkowski et al. [*Biochemistry* (1999) 38:11643-11650], which teaches that only a single amino acid substitution results in conversion of the parent polypeptide's activity from a beta-ketoacyl synthase to a malonyl decarboxylase (see e.g., Table 1, page 11647).

*The amount of direction provided by the inventor and The existence of working*

*examples:* The specification discloses how to make and use only a single working example of the claimed polypeptide, *i.e.*, SEQ ID NO:2. While it is acknowledged that the specification discloses a SEQ ID NO:2 variant, *i.e.*, SEQ ID NO:2 with a single mutation, wherein the mutation is an Asp to Ala mutation at position 2331, it is unclear

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as to how a skilled artisan is to use this disclosed polypeptide. Other than the single working example of SEQ ID NO:2, the specification fails to disclose any specific guidance for altering the amino acid sequence of SEQ ID NO:2 with an expectation that the resulting variants of SEQ ID NO:2 as encompassed by the claims will achieve or maintain the desired activity/utility.

*The quantity of experimentation needed to make or use the invention based on the content of the disclosure:* While methods of isolating or generating variants of a polypeptide were known in the art at the time of the invention, it was not routine in the art to screen – by a trial and error process – for all polypeptide variants having a substantial number of modifications as encompassed by the claims for those polypeptides having the desired activity/utility.

In view of the overly broad scope of the claims, the lack of guidance and working examples provided in the specification, the high level of unpredictability, and the quantity of experimentation, undue experimentation would be necessary for a skilled artisan to make and use the entire scope of the claimed invention. Applicants have not provided sufficient guidance to enable one of ordinary skill in the art to make and use the claimed invention in a manner reasonably correlated with the scope of the claims. The scope of the claims must bear a reasonable correlation with the scope of enablement (*In re Fisher*, 166 USPQ 19 24 (CCPA 1970)). Without sufficient guidance, determination of having the desired biological characteristics is unpredictable and the experimentation left to those skilled in the art is unnecessarily, and improperly,

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extensive and undue. See *In re Wands* 858 F.2d 731, 8 USPQ2nd 1400 (Fed. Cir, 1988).

### ***Claim Rejections - 35 USC § 102***

The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

A person shall be entitled to a patent unless –

(a) the invention was known or used by others in this country, or patented or described in a printed publication in this or a foreign country, before the invention thereof by the applicant for a patent.

(b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.

(e) the invention was described in a patent granted on an application for patent by another filed in the United States before the invention thereof by the applicant for patent, or on an international application by another who has fulfilled the requirements of paragraphs (1), (2), and (4) of section 371(c) of this title before the invention thereof by the applicant for patent.

**[18]** Claims 1-2 and 16-17 are rejected under 35 U.S.C. 102(a) as being anticipated by Denning et al. [*J Biol Chem* (2001) 276:22709-22714; cited as reference CG in the IDS filed 9 August 2004] as evidenced by GenBank Accession Number AY014957. Applicant's attention is directed to the upper right-hand corner of page 22709 of Denning et al., which states, "[p]ublished, JBC Papers in Press, April 30, 2001." According to the "JBC Papers in Press" website ([www.jbc.org/pips/index.dtl](http://www.jbc.org/pips/index.dtl); viewed on February 13, 2006), "***JBC Papers in Press***...will establish publication priority" (emphasis in original).

Initially, it is noted that claim 2 recites "a 90% or more homology," wherein the term "homology" is defined in the specification as "a value obtained by BLAST [Basic

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local alignment search tool; Altschul, S. F. et al., J. Mol. Biol., 215, 403-410, (1990)]” (specification at p. 16, top). As BLAST can be used to determine *similarity* between two sequences, in accordance with MPEP 2111.01, which states (in relevant part), “[d]uring examination, the claims must be interpreted as broadly as their terms reasonably allow,” the term “homology” has been interpreted as similarity between two sequences.

The claims are drawn to variants of SEQ ID NO:2 having SMG-1 activity (claims 1-2), an agent thereof (claim 17), and an agent for suppressing NMD comprising an SMG-1 mutant (claim 16).

Denning et al. teaches isolation of an SMG-1 polypeptide, which has the ability to phosphorylate Upf1p (p. 22713, Figure 4) or kinase-deficient SMG-1 mutants (p. 22710, right column, middle) and teaches the GenBank Accession Number of the encoding nucleic acid, *i.e.*, AY014957 (p. 22709, bottom, left). The polypeptide encoded by Accession Number AY014957 is 99.7% similar to SEQ ID NO:2 (see Appendix A).

This anticipates claims 1-2 and 16-17 as written.

While it is acknowledged that Denning et al. does not teach the polypeptide as being useful for “suppressing nonsense-mediated mRNA decay” or for “promoting nonsense-mediated mRNA decay,” it is noted that if the prior art structure is capable of performing the intended use, then it meets the claim. See MPEP 2111.02.II.

**[19]** Claims 1-3 and 16-17 are rejected under 35 U.S.C. 102(a) as being anticipated by Ohnishi et al. (“23<sup>rd</sup> Annual Meeting of the Molecular Biology Society of Japan,”



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Program and Abstracts, December 14, 2000; cited as reference CB in the IDS filed 9 August 2004).

Claims 1-2 and 16-17 are drawn to polypeptides and agents as described above. Claim 3 is drawn to a polypeptide consisting of SEQ ID NO:2.

The reference of Ohnishi et al. teaches cloning of a human SMG-1 polypeptide (Figure 1A) isolated from HeLa cells that is 400 or 430 kDa (Figure 3 and description thereof), which is disclosed as having kinase activity (Figure 4 and description thereof). A visual comparison of the sequences of SMG-1 as reported by Ohnishi et al. and SEQ ID NO:2 herein indicates that the sequences are identical. This anticipates claims 1-3 and 16-17 as written.

While it is acknowledged that Ohnishi et al. does not teach the polypeptide as being useful for "suppressing nonsense-mediated mRNA decay" or for "promoting nonsense-mediated mRNA decay," it is noted that if the prior art structure is capable of performing the intended use, then it meets the claim. See MPEP 2111.02.II. Since the Office does not have the facilities for examining and comparing applicant's protein with the protein of the prior art, the burden is on the applicant to show a novel or unobvious difference between the claimed product and the product of the prior art (i.e., that the protein of the prior art does not possess the same material structural and functional characteristics of the claimed protein). See *In re Best*, 562 F.2d 1252, 195 USPQ 430 (CCPA 1977) and *In re Fitzgerald et al.*, 205 USPQ 594.

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**[20]** Claims 1-3 and 16-17 are rejected under 35 U.S.C. 102(a) as being anticipated by Yamashita et al. (*Genes Develop* 15:2215-2228, 2001; cited as reference CH in the IDS filed 9 August 2004).

Claims 1-3 and 16-17 are drawn to polypeptides and agents as described above.

The reference of Yamashita et al. teaches cloning of a human SMG-1 polypeptide (Figure 1A) isolated from HeLa cells that is 430 kDa (p. 2218, left column, top), which is disclosed as having kinase activity (p. 2218, right column, bottom). The polypeptide of Yamashita et al. is 100% identical to SEQ ID NO:2 herein (see Appendix B). This anticipates claims 1-3 and 16-17 as written.

While it is acknowledged that Ohnishi et al. does not teach the polypeptide as being useful for "suppressing nonsense-mediated mRNA decay" or for "promoting nonsense-mediated mRNA decay," it is noted that if the prior art structure is capable of performing the intended use, then it meets the claim. See MPEP 2111.02.II. Since the Office does not have the facilities for examining and comparing applicant's protein with the protein of the prior art, the burden is on the applicant to show a novel or unobvious difference between the claimed product and the product of the prior art (i.e., that the protein of the prior art does not possess the same material structural and functional characteristics of the claimed protein). See *In re Best*, 562 F.2d 1252, 195 USPQ 430 (CCPA 1977) and *In re Fitzgerald et al.*, 205 USPQ 594.

**[21]** Claims 1-3 and 16-17 are rejected under 35 U.S.C. 102(b) as being anticipated by Ohnishi et al. ("22<sup>nd</sup> Annual Meeting of the Molecular Biology Society of Japan,"

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Program and Abstracts, December 7-10, 1999; cited as reference CC in the IDS filed 3 August 2006).

Claims 1-3 and 16-17 are drawn to polypeptides and agents as described above.

The reference of Ohnishi et al. teaches immunoprecipitation of a polypeptide referred to as "LICK" from HeLa cell extract (slide 2, part B), which is identified by the reference as being 400 or 430 kDa having kinase activity (abstract) and having an internal sequence that is 100% identical to amino acids 2331 to 2356 of SEQ ID NO:2 herein. This anticipates claims 1-3 and 16-17 as written.

While it is acknowledged that Ohnishi et al. does not teach the entire sequence of LICK, applicant's attention is directed to MPEP 2112, wherein the Court in *In re Crish*, 393 F.3d 1253, 1258, 73 USPQ2d 1364, held that "the claimed promoter sequence obtained by sequencing a prior art plasmid that was not previously sequenced was anticipated by the prior art plasmid which necessarily possessed the same DNA sequence as the claimed oligonucleotides. The court stated that 'just as the discovery of properties of a known material does not make it novel, the identification and characterization of a prior art material also does not make it novel.'" In this case, the polypeptide of Ohnishi et al. and the polypeptide of SEQ ID NO:2 are both disclosed *inter alia* as being isolated from HeLa cells, being 400 or 430 kDa, having kinase activity, and having an identical internal sequence as noted above (pp. 48-49 and 57-58 and sequence listing for SEQ ID NO:2). As such, it is the examiner's position that the polypeptide of Ohnishi et al. is SEQ ID NO:2. If applicant traverses the instant rejection on the grounds that Ohnishi et al. does not demonstrate that the disclosed polypeptide

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has "SMG-1 activity" as defined in the specification (p. 6, lines 17-20), it is noted that this is an inherent feature of the polypeptide of Ohnishi et al. Also, while it is acknowledged that Ohnishi et al. does not teach the polypeptide as being useful for "suppressing nonsense-mediated mRNA decay" or for "promoting nonsense-mediated mRNA decay," it is noted that if the prior art structure is capable of performing the intended use, then it meets the claim. See MPEP 2111.02.II. Since the Office does not have the facilities for examining and comparing applicant's protein with the protein of the prior art, the burden is on the applicant to show a novel or unobvious difference between the claimed product and the product of the prior art (i.e., that the protein of the prior art does not possess the same material structural and functional characteristics of the claimed protein). See *In re Best*, 562 F.2d 1252, 195 USPQ 430 (CCPA 1977) and *In re Fitzgerald et al.*, 205 USPQ 594.

**[22]** Claims 1-2 and 16-17 are rejected under 35 U.S.C. 102(e) as being anticipated by Loughney et al. (US Patent 6,344,549).

The claims are drawn to polypeptides and agents as described above.

Loughney et al. teaches isolation of a kinase polypeptide, SEQ ID NO:2, which has 99.9% similarity to SEQ ID NO:2 herein (see Appendix C). Loughney et al. teaches the polypeptide is most closely related to *C. elegans* SMG-1 (column 32).

This anticipates claims 1-2 and 16-17 as written.

If applicant traverses the instant rejection on the grounds that Loughney et al. does not demonstrate that the disclosed polypeptide has "SMG-1 activity" as defined in

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the specification (p. 6, lines 17-20), it is noted that this is an inherent feature of the polypeptide of SEQ ID NO:2 of Loughney et al. Also, while it is acknowledged that Loughney et al. does not teach the polypeptide as being useful for "suppressing nonsense-mediated mRNA decay" or for "promoting nonsense-mediated mRNA decay," it is noted that if the prior art structure is capable of performing the intended use, then it meets the claim. See MPEP 2111.02.II. Since the Office does not have the facilities for examining and comparing applicant's protein with the protein of the prior art, the burden is on the applicant to show a novel or unobvious difference between the claimed product and the product of the prior art (i.e., that the protein of the prior art does not possess the same material structural and functional characteristics of the claimed protein). See *In re Best*, 562 F.2d 1252, 195 USPQ 430 (CCPA 1977) and *In re Fitzgerald et al.*, 205 USPQ 594.

### ***Conclusion***

**[23]** Status of the claims:

Claims 1-14 and 16-20 are pending.

Claims 4-14 and 18-19 are withdrawn from consideration.

Claims 1-3, 16-17, and 20 are rejected.


No claim is in condition for allowance.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to David J. Steadman whose telephone number is 571-272-0942. The examiner can normally be reached on Monday to Thursday, 6:30 am to 5:00 pm.

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If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Kathleen Kerr can be reached at 571-272-0931. The fax phone number for the organization where this application or proceeding is assigned is 571-273-8300.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see <http://pair-direct.uspto.gov>. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).



David J. Steadman, Ph.D.  
Primary Examiner  
Art Unit 1656

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**APPENDIX A**

AY014957  
LOCUS AY014957 11036 bp mRNA linear PRI 18-JUN-2001  
DEFINITION Homo sapiens PI-3-kinase-related kinase SMG-1 (SMG1) mRNA, complete cds.  
ACCESSION AY014957  
VERSION AY014957.1 GI:14132743  
KEYWORDS .  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 11036)  
AUTHORS Denning, G., Jamieson, L., Maquat, L.E., Thompson, E.A. and Fields, A.P.  
TITLE Cloning of a novel phosphatidylinositol kinase-related kinase: characterization of the human SMG-1 RNA surveillance protein  
JOURNAL J. Biol. Chem. 276 (25), 22709-22714 (2001)  
PUBMED 11331269  
REFERENCE 2 (bases 1 to 11036)  
AUTHORS Denning, G., Jamieson, L. and Fields, A.P.  
TITLE Direct Submission  
JOURNAL Submitted (28-NOV-2000) Human Biological Chemistry and Genetics, The University of Texas Medical Branch, 301 University Blvd., Galveston, TX 77555, USA  
FEATURES  
source Location/Qualifiers  
1. .11036  
/organism="Homo sapiens"  
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/db\_xref="taxon:9606"  
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CDS 133. .9228  
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ORIGIN

Alignment Scores:

Pred. No.:	0	Length:	11036
Score:	15696.50	Matches:	3062
Percent Similarity:	99.71%	Conservative:	4
Best Local Similarity:	99.58%	Mismatches:	2
Query Match:	83.74%	Indels:	7
DB:	8	Gaps:	1

US-10-720-460-2 (1-3657) x AY014957 (1-11036)

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Qy	610	AspLeuSer-----AlaLeuThrThrIleGlyAsnAlaLysAsn	622
Db	61	GACCTCAATTGACTACAAAATTGTAGTTAAATTTGACTACAATTGGAAATGCCAAAAAC	120
Qy	623	SerLeuIleGlyMetTrpAlaLeuSerProThrValPheAlaLeuLeuSerLysAsnLeu	642
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Qy	643	MetIleValHisSerAspLeuAlaValHisPheProAlaIleGlnTyrAlaValLeuTyr	662
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Qy	663	ThrLeuTyrSerHisCysThrArgHisAspHisPheIleSerSerSerLeuSerSerAla	682
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Qy	683	SerProSerLeuPheAspGlyAlaValIleSerThrValThrThrAlaThrLysLysHis	702
Db	301	TCTCCTTCTTTGTTTGATGGAGCTGTGATTAGCACTGTAACACGGCTACAAAGAAACAT	360
Qy	703	PheSerIleIleLeuAsnLeuLeuGlyIleLeuLeuLysLysAspAsnLeuAsnGlnAsp	722
Db	361	TTCTCAATTATATAAATCTTCTGGGAATATTACTTAAGAAAGATAACCTTAACCAGGAC	420
Qy	723	ThrArgLysLeuLeuMetThrTrpAlaLeuGluAlaAlaValLeuMetArgLysSerGlu	742



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|||||:|
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Qy	1343	ProValLeuSerThrLeuGlnLeuTyrCysSerSerAlaLeuGluAsnThrValSerAsn	1362
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Qy	1363	ArgLeuSerThrGluAspCysLeuIleProLeuPheSerGluAlaLeuArgSerCysLys	1382
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Qy	1403	LeuGluLysIleLysGluGlnThrValProIleArgSerHisLeuMetGluLeuGlyLeu	1422
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Qy	1443	GlnCysSerGluValGlnLeuGlyLysThrThrThrAlaGlnAspLeuValGlnHisPhe	1462
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Qy	1583	GluSerThrValHisIleGlyValGlyGluProAspPheIleLeuGlyGlnLeuTyrHis	1602
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Qy	1603	LeuSerSerValGlnAlaProGluValAlaLysSerTrpAlaAlaLeuAlaSerTrpAla	1622
Db	3061	CTGTCTTCAGTACAGGCACCTGAAGTAGCCAAATCTTGGGCAGCGTTGGCCAGCTGGGCT	3120
Qy	1623	TyrArgTrpGlyArgLysValValAspAsnAlaSerGlnGlyGluGlyValArgLeuLeu	1642
Db	3121	TATAGTGGGGCAGAAAGGTGGTTGACAATGCCAGTCAGGGAGAAGGTGTTCTGCTGCTG	3180
Qy	1643	ProArgGluLysSerGluValGlnAsnLeuLeuProAspThrIleThrGluGluGluLys	1662
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Qy	1663	GluArgIleTyrGlyIleLeuGlyGlnAlaValCysArgProAlaGlyIleGlnAspGlu	1682
Db	3241	GAGAGAATATATGGTATTCTTGGACAGGCTGTGTGTCGGCCGGCGGGGATTTCAGGATGAA	3300
Qy	1683	AspIleThrLeuGlnIleThrGluSerGluAspAsnGluGluAspAspMetValAspVal	1702
Db	3301	GATATAACACTTCAGATAACTGAGAGTGAAGACAACGAAGAAGATGACATGGTTGATGTT	3360
Qy	1703	IleTrpArgGlnLeuIleSerSerCysProTrpLeuSerGluLeuAspGluSerAlaThr	1722
Db	3361	ATCTGGCGTCAGTTGATATCAAGCTGCCCATGGCTTTCAGAACTTGATGAAAGTCAACT	3420
Qy	1723	GluGlyValIleLysValTrpArgLysValValAspArgIlePheSerLeuTyrLysLeu	1742

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Db 3721 TTCTCACGCTTAAACCACCCTGAAGTGTATGTGCGCAAAGTATTTGTAACCTTCTCTGC 3780

Qy 1843 ArgValAlaGlnAspSerProHisLeuIleLeuTyrProAlaIleValGlyThrIleSer 1862  
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|||||

Db 3901 GGCAATATTCAAGGAGAAGATTGCTGGTTTCTGAATGTGAGGGAGGAAGTCTCTGCA 3960

Qy 1903 SerGlnAspSerAsnLysAspGluProLysSerGlyLeuAsnGluAspGlnAlaMetMet 1922  
|||||

Db 3961 TCTCAGGATAGCAATAAGGATGAACCTAAAAGTGATTAAATGAAGACCAAGCCATGATG 4020

Qy 1923 GlnAspCysTyrSerLysIleValAspLysLeuSerSerAlaAsnProThrMetValLeu 1942  
|||||

Db 4021 CAGGATTGTTACAGCAAAATTGTAGATAAGCTGTCTCTGCAAAACCCACCATTGTTATTA 4080

Qy 1943 GlnValGlnMetLeuValAlaGluLeuArgArgValThrValLeuTrpAspGluLeuTrp 1962  
|||||

Db 4081 CAGGTTCAGATGCTCGTGGCTGAACTGCGCAGGGTCACTGTGCTCTGGGATGAGCTCTGG 4140

Qy 1963 LeuGlyValLeuLeuGlnGlnHisMetTyrValLeuArgArgIleGlnGlnLeuGluAsp 1982  
|||||

Db 4141 CTGGGAGTTTGTCTGCAACAACACATGTATGTCTGAGACGAATTCAGCAGCTTGAAGAT 4200

Qy 1983 GluValLysArgValGlnAsnAsnAsnThrLeuArgLysGluGluLysIleAlaIleMet 2002  
|||||

Db 4201 GAGGTGAAGAGAGTCCAGAACAACAACACCTTACGCAAGAAGAGAAAATTGCAATCATG 4260

Qy 2003 ArgGluArgHisThrAlaLeuMetLysProIleValPheAlaLeuGluHisValArgSer 2022  
:::|||||

Db 4261 AGGGAGAAGCACACAGCTTTGATGAAGCCCATCGTATTGCTTTGGAGCATGTGAGGAGT 4320

Qy 2023 IleThrAlaAlaProAlaGluThrProHisGluLysTrpPheGlnAspAsnTyrGlyAsp 2042  
|||||

Db 4321 ATCACAGCGGCTCCTGCAGAAACACCTCATGAAAAATGGTTTCAGGATAACTATGGTGAT 4380

Qy 2043 AlaIleGluAsnAlaLeuGluLysLeuLysThrProLeuAsnProAlaLysProGlySer 2062  
|||||

Db 4381 GCCATTGAAAATGCCCTAGAAAACTGAAGACTCCATTGAACCTGCAAAGCCTGGGAGC 4440

Qy 2063 SerTrpIleProPheLysGluIleMetLeuSerLeuGlnGlnArgAlaGlnLysArgAla 2082

Art Unit: 1656

Db 4441 AGCTGGATTCCATTTAAAGAGATAATGCTAAGTTTGCAACAGAGAGCACAGAAACGTGCA 4500  
Qy 2083 SerTyrIleLeuArgLeuGluGluIleSerProTrpLeuAlaAlaMetThrAsnThrGlu 2102  
Db 4501 AGTTACATCTTGCGTCTTGAAGAAATCAGTCCATGGTTGGCTGCCATGACTAACACTGAA 4560  
Qy 2103 IleAlaLeuProGlyGluValSerAlaArgAspThrValThrIleHisSerValGlyGly 2122  
Db 4561 ATTGCTCTTCTGGGGAAGTCTCAGCCAGAGACACTGTCACAATCCATAGTGTGGGCGGA 4620  
Qy 2123 ThrIleThrIleLeuProThrLysThrLysProLysLysLeuLeuPheLeuGlySerAsp 2142  
Db 4621 ACCATCACAATCTTACCGACTAAAACCAAGCCAAAGAAACTTCTCTTCTTGGATCAGAT 4680  
Qy 2143 GlyLysSerTyrProTyrLeuPheLysGlyLeuGluAspLeuHisLeuAspGluArgIle 2162  
Db 4681 GGGGAAGAGCTATCCTTATCTTTCAAAGGACTGGAGGATTTACATCTGGATGAGAGAATA 4740  
Qy 2163 MetGlnPheLeuSerIleValAsnThrMetPheAlaThrIleAsnArgGlnGluThrPro 2182  
Db 4741 ATGCAGTTCCTATCTATTGTGAATACCATGTTTGCTACAATTAATCGCCAAGAAACACCC 4800  
Qy 2183 ArgPheHisAlaArgHisTyrSerValThrProLeuGlyThrArgSerGlyLeuIleGln 2202  
Db 4801 CGGTTCCATGTCGACACTATTCTGTAAACCACTAGGAACAAGATCAGGACTAATCCAG 4860  
Qy 2203 TrpValAspGlyAlaThrProLeuPheGlyLeuTyrLysArgTrpGlnGlnArgGluAla 2222  
Db 4861 TGGGTAGATGGAGCCACACCCTTATTTGGTCTTTACAAACGATGGCAACAACGGGAAGCT 4920  
Qy 2223 AlaLeuGlnAlaGlnLysAlaGlnAspSerTyrGlnThrProGlnAsnProGlyIleVal 2242  
Db 4921 GCCTTACAAGCACAAAAGGCCAAGATTCTTACCAAACTCCTCAGAATCCTGGAATTGTA 4980  
Qy 2243 ProArgProSerGluLeuTyrTyrSerLysIleGlyProAlaLeuLysThrValGlyLeu 2262  
Db 4981 CCCCCTCCTAGTGAACCTTATTACAGTAAATTTGGCCCTGCTTTGAAAACAGTTGGGCTT 5040  
Qy 2263 SerLeuAspValSerArgArgAspTrpProLeuHisValMetLysAlaValLeuGluGlu 2282  
Db 5041 AGCCTGGATGTGTCCCGTCGGGATTGGCCTCTTCATGTAATGAAGGCAGTATTGGAAGAG 5100  
Qy 2283 LeuMetGluAlaThrProProAsnLeuLeuAlaLysGluLeuTrpSerSerCysThrThr 2302  
Db 5101 TTAATGAGGCCACACCCCGAATCTCCTTGCCAAAGAGCTCTGGTCATCTTGCACAACA 5160  
Qy 2303 ProAspGluTrpTrpArgValThrGlnSerTyrAlaArgSerThrAlaValMetSerMet 2322  
Db 5161 CCTGATGAATGGTGGAGAGTTACGCAGTCTTATGCAAGATCTACTGCAGTCATGTCTATG 5220  
Qy 2323 ValGlyTyrIleIleGlyLeuGlyAspArgHisLeuAspAsnValLeuIleAspMetThr 2342  
Db 5221 GTTGGATACATAATTGGCCTTGAGACAGACATCTGGATAATGTTCTTATAGATATGACG 5280  
Qy 2343 ThrGlyGluValValHisIleAspTyrAsnValCysPheGluLysGlyLysSerLeuArg 2362  
Db 5281 ACTGGAGAAGTTGTTACATAGATTACAATGTTTGGCTTTGAAAAAGGTAAAAGCCTTAGA 5340  
Qy 2363 ValProGluLysValProPheArgMetThrGlnAsnIleGluThrAlaLeuGlyValThr 2382  
Db 5341 GTTCCTGAGAAAGTACCTTTTCGAATGACACAAAACATTGAAACAGCACTGGGTGTAAC 5400  
Qy 2383 GlyValGluGlyValPheArgLeuSerCysGluGlnValLeuHisIleMetArgArgGly 2402  
Db 5401 GGAGTAGAAGGTGTATTTAGGCTTTCATGTGAGCAGGTTTTACACATTATGCGGCGTGGC 5460

Qy	2403	ArgGluThrLeuLeuThrLeuLeuGluAlaPheValTyrAspProLeuValAspTrpThr	2442
Db	5461	 AGAGAGACCCTGCTGACGCTGCTGGAGGCCCTTGTGTACGACCCTCTGGTGGACTGGACA	5520
Qy	2423	AlaGlyGlyGluAlaGlyPheAlaGlyAlaValTyrGlyGlyGlyGlnGlnAlaGlu	2442
Db	5521	 GCAGGAGGCGAGGCTGGGTTTGTCTGGTCTGTCTATGGTGGAGGTGGCCAGAGGCCGAG	5580
Qy	2443	SerLysGlnSerLysArgGluMetGluArgGluIleThrArgSerLeuPheSerSerArg	2462
Db	5581	 AGCAAGCAGAGCAAGAGAGAGATGGAGCGAGAGATCACCCGACGCTGTTTTCTTCTAGA	5640
Qy	2463	ValAlaGluIleLysValAsnTrpPheLysAsnArgAspGluMetLeuValValLeuPro	2482
Db	5641	 GTAGCTGAGATTAAGGTGAAGTGGTTTAAAGATAGAGATGAGATGCTGGTTGTGCTTCCC	5700
Qy	2483	LysLeuAspGlySerLeuAspGluTyrLeuSerLeuGlnGluGlnLeuThrAspValGlu	2502
Db	5701	 AAGTTGGACGGTAGCTTAGATGAATACCTAAGCTTGCAAGAGCAACTGACAGATGTGGAA	5760
Qy	2503	LysLeuGlnGlyLysLeuLeuGluGluIleGluPheLeuGluGlyAlaGluGlyValAsp	2522
Db	5761	 AAACTGCAGGGCAAACACTACTGGAGGAAATAGAGTTTCTAGAAGGAGCTGAAGGGGTGGAT	5820
Qy	2523	HisProSerHisThrLeuGlnHisArgTyrSerGluHisThrGlnLeuGlnThrGlnGln	2542
Db	5821	 CATCCTTCTCATACTCTGCAACACAGGTATTCTGAGCACACCCAACACAGACTCAGCAA	5880
Qy	2543	ArgAlaValGlnGluAlaIleGlnValLysLeuAsnGluPheGluGlnTrpIleThrHis	2562
Db	5881	 AGAGCTGTTTCAGGAAGCAATCCAGGTGAAGCTGAATGAATTGAACAAATGGATAACACAT	5940
Qy	2563	TyrGlnAlaAlaPheAsnAsnLeuGluAlaThrGlnLeuAlaSerLeuLeuGlnGluIle	2582
Db	5941	 TATCAGGCTGCATTCAATAATTTAGAAGCAACACAGCTTGCAAGCTTGCTTCAAGAGATA	6000
Qy	2583	SerThrGlnMetAspLeuGlyProProSerTyrValProAlaThrAlaPheLeuGlnAsn	2602
Db	6001	 AGCACACAAATGGACCTTGGTCTCCAAGTTACGTGCCAGCAACAGCCTTTCTGCAGAAT	6060
Qy	2603	AlaGlyGlnAlaHisLeuIleSerGlnCysGluGlnLeuGluGlyGluValGlyAlaLeu	2622
Db	6061	 GCTGGTCAGGCCCACTTGATTAGCCAGTGCGAGCAGCTGGAGGGGGAGGTTGGTGTCTCTC	6120
Qy	2623	LeuGlnGlnArgArgSerValLeuArgGlyCysLeuGluGlnLeuHisHisTyrAlaThr	2642
Db	6121	 CTGCAGCAGAGGCGCTCCGTGTCTCCGTGGCTGTCTGGAGCAACTGCATCACTATGCAACC	6180
Qy	2643	ValAlaLeuGlnTyrProLysAlaIlePheGlnLysHisArgIleGluGlnTrpLysThr	2662
Db	6181	 GTGGCCCTGCAGTATCCGAAGGCCATATTTCAGAAACATCGAATTGAACAGTGAAGACC	6240
Qy	2663	TrpMetGluGluLeuIleCysAsnThrThrValGluArgCysGlnGluLeuTyrArgLys	2682
Db	6241	 TGGATGGAAGAGCTCATCTGTAAACACACAGTAGAGCGTTGTCAAGAGCTCTATAGGAAA	6300
Qy	2683	TyrGluMetGlnTyrAlaProGlnProProProThrValCysGlnPheIleThrAlaThr	2702
Db	6301	 TATGAAATGCAATATGCTCCCCAGCCACCCCCAACAGTGTGTGAGTTCATCACTGCCACT	6360
Qy	2703	GluMetThrLeuGlnArgTyrAlaAlaAspIleAsnSerArgLeuIleArgGlnValGlu	2722
Db	6361	 GAAATGACCCTGCAGCGATACGCAGCAGACATCAACAGCAGACTTATTAGACAAGTGGA	6420
Qy	2723	ArgLeuLysGlnGluAlaValThrValProValCysGluAspGlnLeuLysGluIleGlu	2742
Db	6421	 CGCTTGAAACAGGAAGCTGTCTACTGTGCCAGTTTGTGAAGATCAGTTGAAAGAAATTGAA	6480

Qy	2743	ArgCysIleLysValPheLeuHisGluAsnGlyGluGluGlySerLeuSerLeuAlaSer	2762
Db	6481	CGTTGCATTAAAGTTTTCCTTCATGAGAATGGAGAAGAAGGATCTTTGAGTCTAGCAAGT	6540
Qy	2763	ValIleIleSerAlaLeuCysThrLeuThrArgArgAsnLeuMetMetGluGlyAlaAla	2782
Db	6541	GTTATTATTTCTGCCCTTTGTACCCTTACAAGGCGTAACCTGATGATGGAAGGTGCAGCG	6600
Qy	2783	SerSerAlaGlyGluGlnLeuValAspLeuThrSerArgAspGlyAlaTrpPheLeuGlu	2802
Db	6601	TCAAGTGCTGGAGAACAGCTGGTTGATCTGACTTCTCGGGATGGAGCTGGTTCTTGAG	6660
Qy	2803	GluLeuCysSerMetSerGlyAsnValThrCysLeuValGlnLeuLeuLysGlnCysHis	2822
Db	6661	GAACTCTGCAGTATGAGCGGAAACGTACCTGCTTGTTTCAGTTACTGAAGCAGTGCCAC	6720
Qy	2823	LeuValProGlnAspLeuAspIleProAsnProMetGluAlaSerGluThrValHisLeu	2842
Db	6721	CTGGTGCCACAGGACTTAGATATCCCGAACCCCATGGAAGCGTCTGAGACAGTTCACTTA	6780
Qy	2843	AlaAsnGlyValTyrThrSerLeuGlnGluLeuAsnSerAsnPheArgGlnIleIlePhe	2862
Db	6781	GCCAATGGAGTGTATACCTCACTTCAGGAATTGAATTGCAATTTCCGGCAAATCATATTT	6840
Qy	2863	ProGluAlaLeuArgCysLeuMetLysGlyGluTyrThrLeuGluSerMetLeuHisGlu	2882
Db	6841	CCAGAAGCACTTCGATGTTTAATGAAAGGGGAATACACGTTAGAAAGTATGCTGCATGAA	6900
Qy	2883	LeuAspGlyLeuIleGluGlnThrThrAspGlyValProLeuGlnThrLeuValGluSer	2902
Db	6901	CTGGACGGTCTTATTGAGCAGACCACCGATGGCGTTCCCCTGCAGACTCTAGTGGAATCT	6960
Qy	2903	LeuGlnAlaTyrLeuArgAsnAlaAlaMetGlyLeuGluGluGluThrHisAlaHisTyr	2922
Db	6961	CTTCAGGCCTACTTAAGAAACGCAGCTATGGGACTGGAAGAAGAAACATGCTCATTAC	7020
Qy	2923	IleAspValAlaArgLeuLeuHisAlaGlnTyrGlyGluLeuIleGlnProArgAsnGly	2942
Db	7021	ATCGATGTTGCCAGACTACTACATGCTCAGTACGGTGAATTAATCCAACCGAGAAATGGT	7080
Qy	2943	SerValAspGluThrProLysMetSerAlaGlyGlnMetLeuLeuValAlaPheAspGly	2962
Db	7081	TCAGTTGATGAAACACCCAAATGTCTAGCTGGCCAGATGCTTTTGGTAGCATTTCGATGGC	7140
Qy	2963	MetPheAlaGlnValGluThrAlaPheSerLeuLeuValGluLysLeuAsnLysMetGlu	2982
Db	7141	ATGTTTGCTCAAGTTGAAACTGCTTTCAGCTTATTAGTTGAAAAGTTGAACAAGATGGAA	7200
Qy	2983	IleProIleAlaTrpArgLysIleAspIleIleArgGluAlaArgSerThrGlnValAsn	3002
Db	7201	ATTC CATAGCTTGGCGAAAGATTGACATCATAAGGGAAGCCAGGAGTACTCAAGTTAAT	7260
Qy	3003	PhePheAspAspAspAsnHisArgGlnValLeuGluGluIlePhePheLeuLysArgLeu	3022
Db	7261	TTTTTTGATGATGATAATCACCGGCAGGTGCTAGAAGAGATTTTCTTTCTAAAAGACTA	7320
Qy	3023	GlnThrIleLysGluPhePheArgLeuCysGlyThrPheSerLysThrLeuSerGlySer	3042
Db	7321	CAGACTATTAAGGAGTTCTTCAGGCTCTGTGGTACCTTTTCTAAAACATTGTCAGGATCA	7380
Qy	3043	SerSerLeuGluAspGlnAsnThrValAsnGlyProValGlnIleValAsnValLysThr	3062
Db	7381	AGTTCACTTGAAGATCAGAATACTGTGAATGGGCCTGTACAGATTGTCAATGTGAAAACC	7440
Qy	3063	LeuPheArgAsnSerCysPheSerGluAspGlnMetAlaLysProIleLysAlaPheThr	3082

## Art Unit: 1656

Db 7441 CTTTTTAGAAACTCTTGTTCAGTGAAGACCAATGGCCAAACCTATCAAGGCATTACACA 7500

Qy 3083 AlaAspPheValArgGlnLeuLeuIleGlyLeuProAsnGlnAlaLeuGlyLeuThrLeu 3102  
|||||

Db 7501 GCTGACTTTGTGAGGCAGCTCTTGATAGGGCTACCCAACCAAGCCCTCGGACTCACACTG 7560

Qy 3103 CysSerPheIleSerAlaLeuGlyValAspIleIleAlaGlnValGluAlaLysAspPhe 3122  
|||||

Db 7561 TGCAGTTTTATCAGTGTCTGGGTGTAGACATCATTGCTCAAGTAGAGGCAAAGGACTTT 7620

Qy 3123 GlyAlaGluSerLysValSerValAspAspLeuCysLysLysAlaValGluHisAsnIle 3142  
|||||

Db 7621 GGTGCCGAAAGCAAAGTTTCTGTGTGATGATCTCTGTAAGAAAGCGGTGGAACATAACATC 7680

Qy 3143 GlnIleGlyLysPheSerGlnLeuValMetAsnArgAlaThrValLeuAlaSerSerTyr 3162  
|||||

Db 7681 CAGATAGGAAGTTCTCTCAGCTGGTTATGAACAGGGCAACTGTGTTAGCAAGTTCTTAC 7740

Qy 3163 AspThrAlaTrpLysLysHisAspLeuValArgArgLeuGluThrSerIleSerSerCys 3182  
|||||

Db 7741 GACTGCTCTGGAAGAAGCATGACTTGGTGCGAAGGCTAGAAACAGTATTTCTTCTTGT 7800

Qy 3183 LysThrSerLeuGlnArgValGlnLeuHisIleAlaMetPheGlnTrpGlnHisGluAsp 3202  
|||||

Db 7801 AAGACAAGCCTGCAGCGGTTTCAGCTGCATATTGCCATGTTTCAGTGGAACATGAAGAT 7860

Qy 3203 LeuLeuIleAsnArgProGlnAlaMetSerValThrProProProArgSerAlaIleLeu 3222  
|||||

Db 7861 CTACTTATCAATAGACCACAAGCCATGTCACTCACACCTCCCCACGGTCTGCTATCCTA 7920

Qy 3223 ThrSerMetLysLysLysLeuHisThrLeuSerGlnIleGluThrSerIleAlaThrVal 3242  
|||||

Db 7921 ACCAGCATGAAAAAGAAGCTGCATACCCTGAGCCAGATTGAACTTCTATTGCGACAGTT 7980

Qy 3243 GlnGluLysLeuAlaAlaLeuGluSerSerIleGluGlnArgLeuLysTrpAlaGlyGly 3262  
|||||

Db 7981 CAGGAGAAGCTAGCTGCACTTGAATCAAGTATTGAACAGCGACTCAAGTGGGAGGTGGT 8040

Qy 3263 AlaAsnProAlaLeuAlaProValLeuGlnAspPheGluAlaThrIleAlaGluArgArg 3282  
|||||

Db 8041 GCCAACCTGCATTGGCCCTGTACTACAAGATTTGAAGCAACGATAGCTGAAAGAAGA 8100

Qy 3283 AsnLeuValLeuLysGluSerGlnArgAlaSerGlnValThrPheLeuCysSerAsnIle 3302  
|||||

Db 8101 AATCTTGTCTCTTAAAGAGAGCCAAAGAGCAAGTCAGGTCACATTTCTCTGCAGCAATATC 8160

Qy 3303 IleHisPheGluSerLeuArgThrArgThrAlaGluAlaLeuAsnLeuAspAlaAlaLeu 3322  
|||||

Db 8161 ATTCAATTTGAAAGTTTACGAACAAGAACTGCAGAAGCCTTAAACCTGGATGCGGCGTTA 8220

Qy 3323 PheGluLeuIleLysArgCysGlnGlnMetCysSerPheAlaSerGlnPheAsnSerSer 3342  
|||||

Db 8221 TTTGAACTAATCAAGCGATGTCAAGCAGATGTGTTGTTGTCATCACAGTTTAAACAGTTCA 8280

Qy 3343 ValSerGluLeuGluLeuArgLeuLeuGlnArgValAspThrGlyLeuGluHisProIle 3362  
|||||

Db 8281 GTGTCTGAGTTAGAGCTTCGTTTATTACAGAGAGTGGACACTGGTCTTGAACATCCTATT 8340

Qy 3363 GlySerSerGluTrpLeuLeuSerAlaHisLysGlnLeuThrGlnAspMetSerThrGln 3382  
|||||

Db 8341 GGCAGCTCTGAATGGCTTTTGTGAGCACACAAACAGTTGACCCAGGATATGTCTACTCAG 8400

Qy 3383 ArgAlaIleGlnThrGluLysGluGlnGlnIleGluThrValCysGluThrIleGlnAsn 3402  
|||||

Db 8401 AGGGCAATTTCAGACAGAGAAAGAGCAGCAGATAGAAACGGTCTGTGAAACAATTCAGAA 8460

Qy 3403 LeuValAspAsnIleLysThrValLeuThrGlyHisAsnArgGlnLeuGlyAspValLys 3422



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Db 8461 CTGGTTGATAATATAAAGACTGTGCTCACTGGTCATAACCGACAGCTTGGAGATGTCAA 8520  
Qy 3423 HisLeuLeuLysAlaMetAlaLysAspGluGluAlaAlaLeuAlaAspGlyGluAspVal 3442  
Db 8521 CATCTCTTGAAAGCTATGGCTAAGGATGAAGAAGCTGCTCTGGCAGATGGTGAAGATGTT 8580  
Qy 3443 ProTyrGluAsnSerValArgGlnPheLeuGlyGluTyrLysSerTrpGlnAspAsnIle 3462  
Db 8581 CCCTATGAGAACAGTGTTAGGCAGTTTTTGGGTGAATATAAATCATGGCAAGACAACATT 8640  
Qy 3463 GlnThrValLeuPheThrLeuValGlnAlaMetGlyGlnValArgSerGlnGluHisVal 3482  
Db 8641 CAAACAGTTCTATTTACATTAGTCCAGGCTATGGGTGAGTTCAAGTCAAGAACACGTT 8700  
Qy 3483 GluMetLeuGlnGluIleThrProThrLeuLysGluLeuLysThrGlnSerGlnSerIle 3502  
Db 8701 GAAATGCTCCAGGAAATCACTCCACCTTGAAAGAACTGAAAACACAAAGTCAGAGTATC 8760  
Qy 3503 TyrAsnAsnLeuValSerPheAlaSerProLeuValThrAspAlaThrAsnGluCysSer 3522  
Db 8761 TATAATAATTTAGTGAGTTTTGCATCACCCCTTAGTCACCGATGCAACAAATGAATGTTG 8820  
Qy 3523 SerProThrSerSerAlaThrTyrGlnProSerPheAlaAlaAlaValArgSerAsnThr 3542  
Db 8821 AGTCCAACGTCATCTGCTACTTATCAGCCATCCTTCGCTGCAGCAGTCCGGAGTAACACT 8880  
Qy 3543 GlyGlnLysThrGlnProAspValMetSerGlnAsnAlaArgLysLeuIleGlnLysAsn 3562  
Db 8881 GGCCAGAAAGACTCAGCCTGATGTCATGTCACAGAATGCTAGAAAGCTGATCCAGAAAAAT 8940  
Qy 3563 LeuAlaThrSerAlaAspThrProProSerThrValProGlyThrGlyLysSerValAla 3582  
Db 8941 CTGCTACATCAGCTGATACTCCACCAAGCACCGTTCCAGGAAGTGGCAAGAGTGTGCT 9000  
Qy 3583 CysSerProLysLysAlaValArgAspProLysThrGlyLysAlaValGlnGluArgAsn 3602  
Db 9001 TGTAGTCTCTAAAAGGCAGTCAGAGACCCTAAAAGTGGGAAAGCGGTGCAAGAGAGAAAC 9060  
Qy 3603 SerTyrAlaValSerValTrpLysArgValLysAlaLysLeuGluGlyArgAspValAsp 3622  
Db 9061 TCCTATGCAGTGAGTGTGTGGAAGAGAGTGAAAGCCAAGTTAGAGGGCCGAGATGTTGAT 9120  
Qy 3623 ProAsnArgArgMetSerValAlaGluGlnValAspTyrValIleLysGluAlaThrAsn 3642  
Db 9121 CCGAATAGGAGGATGTCAGTTGCTGAACAGGTTGACTATGTCATTAAGGAAGCAACTAAT 9180  
Qy 3643 LeuAspAsnLeuAlaGlnLeuTyrGluGlyTrpThrAlaTrpVal 3657  
Db 9181 CTAGATAACTTGGCTCAGCTGTATGAAGGTTGGACAGCCTGGGTG 9225

Art Unit: 1656

**APPENDIX B**

Q96Q15 HUMAN

ID Q96Q15\_HUMAN PRELIMINARY; PRT; 3657 AA.  
AC Q96Q15;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Phosphatidylinositol 3-kinase-related protein kinase.  
GN Name=smg-1;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=21429078; PubMed=11544179; DOI=10.1101/gad.913001;  
RA Yamashita A., Ohnishi T., Kashima I., Taya Y., Ohno S.;  
RT "Human SMG-1, a novel phosphatidylinositol 3-kinase-related protein  
RT kinase, associates with components of the mRNA surveillance complex  
RT and is involved in the regulation of nonsense-mediated mRNA decay.";  
RL Genes Dev. 15:2215-2228(2001).  
DR EMBL; AB061371; BAB70696.1; -; mRNA.  
DR Ensembl; ENSG00000157106; Homo sapiens.  
DR GO; GO:0005488; F:binding; IEA.  
DR GO; GO:0016301; F:kinase activity; IEA.  
DR GO; GO:0016773; F:phosphotransferase activity, alcohol group . . . ; IEA.  
DR InterPro; IPR011989; ARM-like.  
DR InterPro; IPR003152; FATC.  
DR InterPro; IPR000357; HEAT.  
DR InterPro; IPR000403; PI3/4\_kinase\_cat.  
DR Pfam; PF02260; FATC; 1.  
DR Pfam; PF02985; HEAT; 1.  
DR Pfam; PF00454; PI3\_PI4\_kinase; 1.  
DR SMART; SM00146; PI3Kc; 1.  
DR PROSITE; PS00916; PI3\_4\_KINASE\_2; 1.  
DR PROSITE; PS0290; PI3\_4\_KINASE\_3; 1.  
KW Kinase.  
SQ SEQUENCE 3657 AA; 410286 MW; 182D59966FD82243 CRC64;

Query Match 100.0%; Score 18745; DB 2; Length 3657;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3657; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSRRAPGSRLLSSGGTNYRSWNWQPRDTSASADPGNLKYSSSRDRGGSSSYGLQPSNSA 60  
Db 1 MSRRAPGSRLLSSGGTNYRSWNWQPRDTSASADPGNLKYSSSRDRGGSSSYGLQPSNSA 60  
Qy 61 VVSRQRHDDTRVHADIQNDKGGYSVNGGSGENTYGRKSLGQELRVNNTVSPEFTSVQHG 120  
Db 61 VVSRQRHDDTRVHADIQNDKGGYSVNGGSGENTYGRKSLGQELRVNNTVSPEFTSVQHG 120  
Qy 121 SRALATKDMRKSQERSMSYSDESRLSNLLRRITREDDRRRLATVKQLKEFIQQPENKLV 180  
Db 121 SRALATKDMRKSQERSMSYSDESRLSNLLRRITREDDRRRLATVKQLKEFIQQPENKLV 180  
Qy 181 LVKQLDNILAAVHVDVLNESSKLLQELRQEGACCLGLLCASLSYEA EKIFKWI FSKFSSSA 240  
Db 181 LVKQLDNILAAVHVDVLNESSKLLQELRQEGACCLGLLCASLSYEA EKIFKWI FSKFSSSA 240  
Qy 241 KDEVKLLYLCAATYKALETVGEKKAFSSVMQLVMTSLQSIENVDTPPELLCKCVKCILLVA 300  
Db 241 KDEVKLLYLCAATYKALETVGEKKAFSSVMQLVMTSLQSIENVDTPPELLCKCVKCILLVA 300  
Qy 301 RCYPHIFSTNFRDVTVDILVGWHIDHTQKPSLTQQVSGWLQSLEPFVWADLAFSTTLGQF 360  
Db 301 RCYPHIFSTNFRDVTVDILVGWHIDHTQKPSLTQQVSGWLQSLEPFVWADLAFSTTLGQF 360  
Qy 361 LEDMEAYAEDLSHVASGESVDEDVPPPSVSLPKLAALLRVFSTVVRSIGERFSPIRGPPI 420  
Db 361 LEDMEAYAEDLSHVASGESVDEDVPPPSVSLPKLAALLRVFSTVVRSIGERFSPIRGPPI 420

Qy	421	TEAYVTDVLYRVMRCVTAANQVVFSEAVLTAANECVGVLLGSLDPSMTIHCDMVITYGLD	480
Db	421	TEAYVTDVLYRVMRCVTAANQVVFSEAVLTAANECVGVLLGSLDPSMTIHCDMVITYGLD	480
Qy	481	QLENCQTCGTDYIIISVLNLLTLIVEQINTKLPSSFVEKLFIPSSKLLFLRYHKEKEVVAV	540
Db	481	QLENCQTCGTDYIIISVLNLLTLIVEQINTKLPSSFVEKLFIPSSKLLFLRYHKEKEVVAV	540
Qy	541	AHAVYQAVLSLKNIPVLETAYKLIIGEMTCALNLLHSLQLPEACSEIKHEAFKNHVFNV	600
Db	541	AHAVYQAVLSLKNIPVLETAYKLIIGEMTCALNLLHSLQLPEACSEIKHEAFKNHVFNV	600
Qy	601	DNAKFVVKFDLSALTTIGNAKNSLIGMWALSPTVFALLSKNLMIVHSDLAHVFPPIQYAV	660
Db	601	DNAKFVVKFDLSALTTIGNAKNSLIGMWALSPTVFALLSKNLMIVHSDLAHVFPPIQYAV	660
Qy	661	LYTLYSHCTRHDHFISSSLSSASPSLFDGAVISTVTTATKKHFSIILNLLGILLKKDNLN	720
Db	661	LYTLYSHCTRHDHFISSSLSSASPSLFDGAVISTVTTATKKHFSIILNLLGILLKKDNLN	720
Qy	721	QDTRKLLMTWALEAAVLMRKSETYAPLFSLPSPHFKCKGLLANTLVEDVNICLQACSSLH	780
Db	721	QDTRKLLMTWALEAAVLMRKSETYAPLFSLPSPHFKCKGLLANTLVEDVNICLQACSSLH	780
Qy	781	ALSSSLPDDLQRCVDVCRVQLVHSGTRIRQAFGKLLKSIPLDVVLSNNNHTEIQEISLA	840
Db	781	ALSSSLPDDLQRCVDVCRVQLVHSGTRIRQAFGKLLKSIPLDVVLSNNNHTEIQEISLA	840
Qy	841	LRSHMSKAPSNTFHPQDFSDVISFILYGNSHRTGKDNWLERLFYSCQRLDKRDQSTIPRN	900
Db	841	LRSHMSKAPSNTFHPQDFSDVISFILYGNSHRTGKDNWLERLFYSCQRLDKRDQSTIPRN	900
Qy	901	LLKTDVAVLWQWAIWEAAQFTVLSKLRTPPLGRAQDTFQTIIEGIRSLAAHTLNPDQDVSWQ	960
Db	901	LLKTDVAVLWQWAIWEAAQFTVLSKLRTPPLGRAQDTFQTIIEGIRSLAAHTLNPDQDVSWQ	960
Qy	961	TTADNDEGHGNNQLRLVLLQLYLENLEKLMYNAYEGCANALTSPPKVI RTFFYTNRQTCQ	1020
Db	961	TTADNDEGHGNNQLRLVLLQLYLENLEKLMYNAYEGCANALTSPPKVI RTFFYTNRQTCQ	1020
Qy	1021	DWLTRIRLSIMRVGLLAGQPAVTVRHGFDLLTEMKTTSLSQGNELEVIMMVVEALCELH	1080
Db	1021	DWLTRIRLSIMRVGLLAGQPAVTVRHGFDLLTEMKTTSLSQGNELEVIMMVVEALCELH	1080
Qy	1081	CPEAIQGIADVSSSIVGKNLLWINSVAQQAEGRFEKASVEYQEHLCAMTGVDCCISSFDK	1140
Db	1081	CPEAIQGIADVSSSIVGKNLLWINSVAQQAEGRFEKASVEYQEHLCAMTGVDCCISSFDK	1140
Qy	1141	SVLTLANAGRNSASPKHSLNGESRKTVLSKPTDSSPEVINYLGNKACEFYISADWAAVQ	1200
Db	1141	SVLTLANAGRNSASPKHSLNGESRKTVLSKPTDSSPEVINYLGNKACEFYISADWAAVQ	1200
Qy	1201	EWQNAIHDLLKKSTSSTSLNLKADFNYIKSLSSSFESGKFVECTEQLELLPGENINLLAGGS	1260
Db	1201	EWQNAIHDLLKKSTSSTSLNLKADFNYIKSLSSSFESGKFVECTEQLELLPGENINLLAGGS	1260
Qy	1261	KEKIDMKKLLPNMLSPDPRELQKSIEVQLLRSSVCLATALNP IEQDKWQSITENVVKYL	1320
Db	1261	KEKIDMKKLLPNMLSPDPRELQKSIEVQLLRSSVCLATALNP IEQDKWQSITENVVKYL	1320
Qy	1321	KQTSRIAIGPLRLSTLTVSQSLPVLSTLQLYCSSALENTVSNRLSTEDCLIPLFSEALRS	1380
Db	1321	KQTSRIAIGPLRLSTLTVSQSLPVLSTLQLYCSSALENTVSNRLSTEDCLIPLFSEALRS	1380
Qy	1381	CKQHDVRPWWQALRYTMYQNQLLEKI KEQTVPIRSHLMELGLTAAKFARKGNVSLATRL	1440
Db	1381	CKQHDVRPWWQALRYTMYQNQLLEKI KEQTVPIRSHLMELGLTAAKFARKGNVSLATRL	1440
Qy	1441	LAQCSEVQLGKTTTAQDLVQHFKKLSLTOGQVDEKWPGLDIEKTKLLYTAGQSTHAMEML	1500
Db	1441	LAQCSEVQLGKTTTAQDLVQHFKKLSLTOGQVDEKWPGLDIEKTKLLYTAGQSTHAMEML	1500

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Qy 1501 SSCAISFCKSVKAEYAVAKSILTLAKWIAEWKEISGQLKQVYRAQHQNFTGLSTLSKN 1560  
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Db 1501 SSCAISFCKSVKAEYAVAKSILTLAKWIAEWKEISGQLKQVYRAQHQNFTGLSTLSKN 1560  
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Qy 1561 ILTLIELPSVNTMEEYPRIESESTVHIGVGEPDFILGQLYHLSSVQAPEVAKSWAALAS 1620  
|||||  
Db 1561 ILTLIELPSVNTMEEYPRIESESTVHIGVGEPDFILGQLYHLSSVQAPEVAKSWAALAS 1620  
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Qy 1621 WAYRWGRKVVDNASQGEVRLLPREKSEVQNLLPDTITEEEKERIYGILGQAVCRPAGIQ 1680  
|||||  
Db 1621 WAYRWGRKVVDNASQGEVRLLPREKSEVQNLLPDTITEEEKERIYGILGQAVCRPAGIQ 1680  
|||||

Qy 1681 DEDITLQITESEDNEEDDMVDVIWRQLISSCPWLSELDESATEGVIKVRKVVDRIFSLY 1740  
|||||  
Db 1681 DEDITLQITESEDNEEDDMVDVIWRQLISSCPWLSELDESATEGVIKVRKVVDRIFSLY 1740  
|||||

Qy 1741 KLSCSAYFTFLKLNAGQIPLDEDDPRLHLSHRVEQSTDDMIVMATLRLRLLVKHAGELR 1800  
|||||  
Db 1741 KLSCSAYFTFLKLNAGQIPLDEDDPRLHLSHRVEQSTDDMIVMATLRLRLLVKHAGELR 1800  
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Qy 1801 QYLEHGLETTPTAPWGGIIPQLFSRLNHPEVYVRQSIENLLCRVAQDSPHLILYPAIVGT 1860  
|||||  
Db 1801 QYLEHGLETTPTAPWGGIIPQLFSRLNHPEVYVRQSIENLLCRVAQDSPHLILYPAIVGT 1860  
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Qy 1861 ISLSSESQASGNKFSTAIPTLGNIQGEELLVSECEGGSPPASQDSNKDEPKSGLNEDQA 1920  
|||||  
Db 1861 ISLSSESQASGNKFSTAIPTLGNIQGEELLVSECEGGSPPASQDSNKDEPKSGLNEDQA 1920  
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Qy 1921 MMQDCYSKIVDKLSSANPTMVLQVQMLVAELRRVTVLWDELWLGVLQQHMYVLRRIQQL 1980  
|||||  
Db 1921 MMQDCYSKIVDKLSSANPTMVLQVQMLVAELRRVTVLWDELWLGVLQQHMYVLRRIQQL 1980  
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Qy 1981 EDEVKRVQNNNTLRKEEKIAIMRERHTALMKPIVFALEHVSITAAPAETPHEKWFQDNY 2040  
|||||  
Db 1981 EDEVKRVQNNNTLRKEEKIAIMRERHTALMKPIVFALEHVSITAAPAETPHEKWFQDNY 2040  
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Qy 2041 GDAIENALEKLTPLNPAKPGSSWIPFKEIMLSLQRAQKRASYILRLLEEISPWLAAMTN 2100  
|||||  
Db 2041 GDAIENALEKLTPLNPAKPGSSWIPFKEIMLSLQRAQKRASYILRLLEEISPWLAAMTN 2100  
|||||

Qy 2101 TEIALPGEVSARDTVTIHSVGGTITILPTKTKPKKLLFLGSDGKSYPYLFGKLEDLHLDE 2160  
|||||  
Db 2101 TEIALPGEVSARDTVTIHSVGGTITILPTKTKPKKLLFLGSDGKSYPYLFGKLEDLHLDE 2160  
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Qy 2161 RIMQFLSIVNTMFATINRQETPRFHARHYSVTPLGTRSGLIQWVDGATPLFGLYKRWQQR 2220  
|||||  
Db 2161 RIMQFLSIVNTMFATINRQETPRFHARHYSVTPLGTRSGLIQWVDGATPLFGLYKRWQQR 2220  
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Qy 2221 EAALQAQKAQDSYQTPQNPGIVPRPSELYYSKIGPALKTVGLSLDVSRRDWPLHVMKAVL 2280  
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Db 2221 EAALQAQKAQDSYQTPQNPGIVPRPSELYYSKIGPALKTVGLSLDVSRRDWPLHVMKAVL 2280  
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Qy 2281 EELMEATPPNLLAKELWSSCTTPDEWWRVTQSYARSTAVMSMVGYIIGLGRHLDNVLID 2340  
|||||  
Db 2281 EELMEATPPNLLAKELWSSCTTPDEWWRVTQSYARSTAVMSMVGYIIGLGRHLDNVLID 2340  
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Qy 2341 MTTGEVVHIDYNVCFEKGKSLRVPEKVPFRMTQNIETALGVTGVEGVFRLSCEQVLHIMR 2400  
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Db 2341 MTTGEVVHIDYNVCFEKGKSLRVPEKVPFRMTQNIETALGVTGVEGVFRLSCEQVLHIMR 2400  
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Qy 2401 RGRETLLTLLEAFVYDPLVDWTAGGEAGFAGAVYGGGQQAESKQSKREMERETRSLSFS 2460  
|||||  
Db 2401 RGRETLLTLLEAFVYDPLVDWTAGGEAGFAGAVYGGGQQAESKQSKREMERETRSLSFS 2460  
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Qy 2461 SRVAEIKVNWFKNRDEMLVVLPKLDGSLDEYLSLQEQLTDEKLQGLLEEIEFLEGAEG 2520  
|||||  
Db 2461 SRVAEIKVNWFKNRDEMLVVLPKLDGSLDEYLSLQEQLTDEKLQGLLEEIEFLEGAEG 2520  
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Qy 2521 VDHPSTLQHRYSEHTQLQTOQRAVQEAIOVKLNEFEQWITHYQAAFNNLEATQLASLLQ 2580  
|||||  
Db 2521 VDHPSTLQHRYSEHTQLQTOQRAVQEAIOVKLNEFEQWITHYQAAFNNLEATQLASLLQ 2580  
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Qy 2581 EISTQMDLGPPSYVPATAFLQNAQQAHLISQCEQLEGEVGALLQORRSVLRGCLEQLHHY 2640  
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Db 2581 EISTQMDLGPPSYVPATAFLQNAQQAHLISQCEQLEGEVGALLQORRSVLRGCLEQLHHY 2640  
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Qy 2641 ATVALQYPKAI FQKHRIEQWKTWMEELICNTTVERCQELYRKYEMQYAPQPPPTVCQFIT 2700  
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Db 2641 ATVALQYPKAI FQKHRIEQWKTWMEELICNTTVERCQELYRKYEMQYAPQPPPTVCQFIT 2700  
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Qy 2701 ATEMTLQRYAADINSRLIRQVERLKQEAVTPVPCEDQLKEIERCIKVFLHENGEEGSLSL 2760  
|||||  
Db 2701 ATEMTLQRYAADINSRLIRQVERLKQEAVTPVPCEDQLKEIERCIKVFLHENGEEGSLSL 2760  
|||||

Qy 2761 ASV IISALCTLTRRNLMMEGAASSAGEQLVDLTSRDGAWFLEELCSMSGNVTCVLQLLKQ 2820  
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Db 2761 ASV IISALCTLTRRNLMMEGAASSAGEQLVDLTSRDGAWFLEELCSMSGNVTCVLQLLKQ 2820  
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Qy 2821 CHLVPQDL DIPNMEASETVHLANGVYTSLQELNSNFRQ IIFPEALRCLMKGEYTLSEML 2880  
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Db 2821 CHLVPQDL DIPNMEASETVHLANGVYTSLQELNSNFRQ IIFPEALRCLMKGEYTLSEML 2880  
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Qy 2881 HELDGLIEQTTDGVPLQTLVESLQAYLRNAAMGLEEETHAHYIDVARLLHAQYGELIQPR 2940  
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Db 2881 HELDGLIEQTTDGVPLQTLVESLQAYLRNAAMGLEEETHAHYIDVARLLHAQYGELIQPR 2940  
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Qy 2941 NGSVDETPKMSAGQMLLVAFDGMFAQVETAFSLLEKLNKMEIPIAWRKID IIREARSTQ 3000  
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Db 2941 NGSVDETPKMSAGQMLLVAFDGMFAQVETAFSLLEKLNKMEIPIAWRKID IIREARSTQ 3000  
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Qy 3001 VNFDDDNHRQVLEEIFFLKRLQTIKEFFRLCGTFSKTLSGSSSLEDQNTVNGPVQIVNV 3060  
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Db 3001 VNFDDDNHRQVLEEIFFLKRLQTIKEFFRLCGTFSKTLSGSSSLEDQNTVNGPVQIVNV 3060  
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Qy 3061 KTLFRNSCFSEDQMAKPIKAFTADFVRQLLIGLPNQAALGLTLC SFISALGVDI IIAQVEAK 3120  
|||||  
Db 3061 KTLFRNSCFSEDQMAKPIKAFTADFVRQLLIGLPNQAALGLTLC SFISALGVDI IIAQVEAK 3120  
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Qy 3121 DFGAESKVSVDLCKKAVEHNIQIGKFSQLVMNRATVLASSYDTAWKKHDLVRRLETSIS 3180  
|||||  
Db 3121 DFGAESKVSVDLCKKAVEHNIQIGKFSQLVMNRATVLASSYDTAWKKHDLVRRLETSIS 3180  
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Qy 3181 SCKTSLQRVQLHIAMFQWQHEDLLINRPQAMSVTPPPRSAILTSMKKKLHTLSQIETSIA 3240  
|||||  
Db 3181 SCKTSLQRVQLHIAMFQWQHEDLLINRPQAMSVTPPPRSAILTSMKKKLHTLSQIETSIA 3240  
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Qy 3241 TVQEKLAALLESSIEQRLKWAGGANPALAPVLQDFEATIAERRNLVLKESQRASQVTFLCS 3300  
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Db 3241 TVQEKLAALLESSIEQRLKWAGGANPALAPVLQDFEATIAERRNLVLKESQRASQVTFLCS 3300  
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Qy 3301 NIIHFESLRTRTAEALNLDAALFELIKRCQQMCSFASQFNSSVSELELRLLQRVDTGLEH 3360  
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Db 3301 NIIHFESLRTRTAEALNLDAALFELIKRCQQMCSFASQFNSSVSELELRLLQRVDTGLEH 3360  
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Qy 3361 PIGSSEWLLSAHKQLTQDMSTQRAIQTEKEQIETVCETIQNLVDNIKT VLTGHNRLQD 3420  
|||||  
Db 3361 PIGSSEWLLSAHKQLTQDMSTQRAIQTEKEQIETVCETIQNLVDNIKT VLTGHNRLQD 3420  
|||||

Qy 3421 VKHLLKAMAKDEEAALADGEDVPYENSVRQFLGEYKSWQDNIQT VLFVLVQAMGQVRSQE 3480  
|||||  
Db 3421 VKHLLKAMAKDEEAALADGEDVPYENSVRQFLGEYKSWQDNIQT VLFVLVQAMGQVRSQE 3480  
|||||

Qy 3481 HVEMLQEITPTLKEKLTQSQSIYNNLVSFASPLVTDATNECSSPTSSATYQPSFAAAVRS 3540  
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Db 3481 HVEMLQEITPTLKEKLTQSQSIYNNLVSFASPLVTDATNECSSPTSSATYQPSFAAAVRS 3540  
|||||

Qy 3541 NTGQKTQPDVMSQNARKLIQKNLATSADTPPSTVPGTGKSVACSPKKAVRDPKTGKAVQE 3600  
|||||  
Db 3541 NTGQKTQPDVMSQNARKLIQKNLATSADTPPSTVPGTGKSVACSPKKAVRDPKTGKAVQE 3600  
|||||

Qy 3601 RNSYAVSVWKRVKAKLEGRDVPNRRMSVAEQVDYVIKEATNLDNLAQLYEGWTAWV 3657  
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Db 3601 RNSYAVSVWKRVKAKLEGRDVPNRRMSVAEQVDYVIKEATNLDNLAQLYEGWTAWV 3657  
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**APPENDIX C**

US-09-417-822-2

; Sequence 2, Application US/09417822

; Patent No. 6344549

; GENERAL INFORMATION:

; APPLICANT: Keegan, Kathy

; TITLE OF INVENTION: ATR-2

; FILE REFERENCE: 27866/35633

; CURRENT APPLICATION NUMBER: US/09/417,822

; CURRENT FILING DATE: 1999-10-14

; NUMBER OF SEQ ID NOS: 43

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 2

; LENGTH: 2930

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-417-822-2

Query Match 80.1%; Score 15023; DB 2; Length 2930;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 2927; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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Qy      728 MTWALEAAVLMRKSETYAPLFSLPSPHFKCKGLLANTLVEDVNICLQACSSLHALSSSLP 787
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Db      1 MTWALEAAVLMKKSETYAPLFSLPSPHFKCKGLLANTLVEDVNICLQACSSLHALSSSLP 60

Qy      788 DDLLQRCVDVCRVQLVHSGTRIRQAFGKLLKSIPLDVVLSNNNHTEIQEISLALRSHMSK 847
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      61 DDLLQRCVDVCRVQLVHSGTRIRQAFGKLLKSIPLDVVLSNNNHTEIQEISLALRSHMSK 120

Qy      848 APSNTFHPQDFSDVISFILYGNSHRTGKDNWLERLFYSCQRLDKRDQSTIPRNLLKTDVAV 907
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      121 APSNTFHPQDFSDVISFILYGNSHRTGKDNWLERLFYSCQRLDKRDQSTIPRNLLKTDVAV 180

Qy      908 LWQWAIWEAAQFTVLSKLRTPLGRAQDTFQTIIEGIIRSLAAHTLNPQDQVSQWTTADNDE 967
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      181 LWQWAIWEAAQFTVLSKLRTPLGRAQDTFQTIIEGIIRSLAAHTLNPQDQVSQWTTADNDE 240

Qy      968 GHGNNQLRLVLLQLYLENLEKLMYNAYEGCANALTSPPKVIRTFYTNRQTCQDWLTRIR 1027
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      241 GHGNNQLRLVLLQLYLENLEKLMYNAYEGCANALTSPPKVIRTFYTNRQTCQDWLTRIR 300

Qy      1028 LSIMRVGGLLAGQPAVTVRHGFDLLTEMKTTSLSQGNELEVTTMMVVEALCELHCPEAIQG 1087
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Db      301 LSIMRVGGLLAGQPAVTVRHGFDLLTEMKTTSLSQGNELEVTTMMVVEALCELHCPEAIQG 360

Qy      1088 IAVWSSSIVGKNLLWINSVAQQAEGRFKASVEYQEHLCAMTGVDCISSFDKSVLTLAN 1147
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      361 IAVWSSSIVGKNLLWINSVAQQAEGRFKASVEYQEHLCAMTGVDCISSFDKSVLTLAN 420

Qy      1148 AGRNSASPKHSLNGESRKTVLSKPTDSSPEVINYLGNKACEFYISIAADWAAVQEWQNAIH 1207
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Db      421 AGRNSASPKHSLNGESRKTVLSKPTDSSPEVINYLGNKACEFYISIAADWAAVQEWQNAIH 480

Qy      1208 DLKKSTSSTSLNLKADFNYIKSLSSFESGKFVECTEQLELLPGENINLLAGGSKEKIDMK 1267
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Db      481 DLKKSTSSTSLNLKADFNYIKSLSSFESGKFVECTEQLELLPGENINLLAGGSKEKIDMK 540

Qy      1268 KLLPNMLSPDPRELQKSIEVQLLRSSVCLATALNPQDQKQWQSITENVVKYLKQTSRIA 1327
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Db      541 KLLPNMLSPDPRELQKSIEVQLLRSSVCLATALNPQDQKQWQSITENVVKYLKQTSRIA 600

Qy      1328 IGPLRLSTLTVSQSLPVLSTLQLYCSSALENTVSNRLSTEDCLIPFSEALRSCKQHDVR 1387
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Db      601 IGPLRLSTLTVSQSLPVLSTLQLYCSSALENTVSNRLSTEDCLIPFSEALRSCKQHDVR 660

Qy      1388 PWMQALRYTMYQNQLLEKIKEQTVPIRSHLMELGLTAAKFARKRGVSLATRLLAQCSEV 1447
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Db 661 PWMQALRYTMYQNQLLEKIKEQTVPIRSHLMELGLTAAKFARKRGVSLATRLLAQCSEV 720

Qy 1448 QLGKTTTAQDLVQHFKKLSTQGQVDEKQWPELDIEKTKLLYTAGQSTHAMEMLSSCAISF 1507

Db 721 QLGKTTTAQDLVQHFKKLSTQGQVDEKQWPELDIEKTKLLYTAGQSTHAMEMLSSCAISF 780

Qy 1508 CKSVKAEYAVAKSILTLAKWIAEWKEISGQLKQVYRAHQHQNFTGLSTLSKNILTLIEL 1567

Db 781 CKSVKAEYAVAKSILTLAKWIAEWKEISGQLKQVYRAHQHQNFTGLSTLSKNILTLIEL 840

Qy 1568 PSVNTMEEYYPRIESESTVHIGVGEPDFILGQLYHLSSVQAPEVAKSWAALASWAYRWGR 1627

Db 841 PSVNTMEEYYPRIESESTVHIGVGEPDFILGQLYHLSSVQAPEVAKSWAALASWAYRWGR 900

Qy 1628 KVVNDASQGEVRLLPREKSEVNLLPDTITEEEKERIYGILGQAVCRPAGIQDEDITLQ 1687

Db 901 KVVNDASQGEVRLLPREKSEVNLLPDTITEEEKERIYGILGQAVCRPAGIQDEDITLQ 960

Qy 1688 ITESEDNEEDDMVDVIWRQLISSCPWLSELDESATEGVIKVRKVVDRIFSLYKLSCSAY 1747

Db 961 ITESEDNEEDDMVDVIWRQLISSCPWLSELDESATEGVIKVRKVVDRIFSLYKLSCSAY 1020

Qy 1748 FTFLKLNAGQIPLDEDDPRLHLSHRVEQSTDDMIVMATLRLRLLVKHAGELRQYLEHGL 1807

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Qy 1808 ETTPTAPWRGIIPQLFSRLNHPEVYVRQSIENLLCRVAQDSPHLILYPAIVGTISLSSES 1867

Db 1081 ETTPTAPWRGIIPQLFSRLNHPEVYVRQSIENLLCRVAQDSPHLILYPAIVGTISLSSES 1140

Qy 1868 QASGNKFSTAIPTLGNIQGEELLVSECEGGSPPASQDSNKDEPKSGLNEDQAMMQDCYS 1927

Db 1141 QASGNKFSTAIPTLGNIQGEELLVSECEGGSPPASQDSNKDEPKSGLNEDQAMMQDCYS 1200

Qy 1928 KIVDKLSSANPTMVLVQVQLVAELRRVTVLWDELWLGVLLQQHMYVLRIQLEDEVKRV 1987

Db 1201 KIVDKLSSANPTMVLVQVQLVAELRRVTVLWDELWLGVLLQQHMYVLRIQLEDEVKRV 1260

Qy 1988 QNNNTLRKEEKIAIMRERHTALMKPIVFALEHVRSTAAETPHEKWFQDNYGDAIENA 2047

Db 1261 QNNNTLRKEEKIAIMREKHTALMKPIVFALEHVRSTAAETPHEKWFQDNYGDAIENA 1320

Qy 2048 LEKLKTPNLPAKPGSSWIPFKEIMLSLQORAQKRASYILRLLEEISPWLAAMTNTETALPG 2107

Db 1321 LEKLKTPNLPAKPGSSWIPFKEIMLSLQORAQKRASYILRLLEEISPWLAAMTNTETALPG 1380

Qy 2108 EVSARDVTIHSVGGTITILPTKTKPKKLLFLGSDGKSYPYLFKGLEDLHLDERIMQFLS 2167

Db 1381 EVSARDVTIHSVGGTITILPTKTKPKKLLFLGSDGKSYPYLFKGLEDLHLDERIMQFLS 1440

Qy 2168 IVNTMFATINRQETPRFHARHYSVTPLGTRSGLIQWVDGATPLFGLYKRWQQREAAALQAA 2227

Db 1441 IVNTMFATINRQETPRFHARHYSVTPLGTRSGLIQWVDGATPLFGLYKRWQQREAAALQAA 1500

Qy 2228 KAQDSYQTPQNPGIVPRPSELYYSKIGPALKTVGLSLDVSRRDWPLHVMKAVLEELMEAT 2287

Db 1501 KAQDSYQTPQNPGIVPRPSELYYSKIGPALKTVGLSLDVSRRDWPLHVMKAVLEELMEAT 1560

Qy 2288 PPNLLAKELWSSCTTPDEWWRVTQSYARSTAVMSMGYIIGLGDRLDNVLDIMTTGEVV 2347

Db 1561 PPNLLAKELWSSCTTPDEWWRVTQSYARSTAVMSMGYIIGLGDRLDNVLDIMTTGEVV 1620

Qy 2348 HIDYNVCFEKGKSLRVPEKVPFRMTQNIETALGVTGVEGVFRLSCEQVLHIMRRGRETLL 2407

Db 1621 HIDYNVCFEKGKSLRVPEKVPFRMTQNIETALGVTGVEGVFRLSCEQVLHIMRRGRETLL 1680

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Qy	2408	TLLEAFVYDPLVDWTAGGEAGFAGAVYGGGQQAESKQSKREMERETRSLSFSSRVAEIK	2467
Db	1681	TLLEAFVYDPLVDWTAGGEAGFAGAVYGGGQQAESKQSKREMERETRSLSFSSRVAEIK	1740
Qy	2468	VNWFKNRDEMLVVLPKLDGSLDEYLSLQEQLTDVEKLQGKLLLEEIEFLEGAEGVDHPSHT	2527
Db	1741	VNWFKNRDEMLVVLPKLDGSLDEYLSLQEQLTDVEKLQGKLLLEEIEFLEGAEGVDHPSHT	1800
Qy	2528	LQHRYSEHTQLQTQQRVQAEIQVKLNEFEQWITHYQAAFNNLEATQLASLLQEISTQMD	2587
Db	1801	LQHRYSEHTQLQTQQRVQAEIQVKLNEFEQWITHYQAAFNNLEATQLASLLQEISTQMD	1860
Qy	2588	LGPPSYVPATAFLQNAQAHLISQCEQLEGEVGALLQQRSSVLRGCLQLHHYATVALQY	2647
Db	1861	LGPPSYVPATAFLQNAQAHLISQCEQLEGEVGALLQQRSSVLRGCLQLHHYATVALQY	1920
Qy	2648	PKAIFQKHRIEQWKTWMEELICNTTVERCQELYRKYEMQYAPQPPPTVCQFITATEMTLQ	2707
Db	1921	PKAIFQKHRIEQWKTWMEELICNTTVERCQELYRKYEMQYAPQPPPTVCQFITATEMTLQ	1980
Qy	2708	RYAADINSRLIRQVERLKQEAVTVPVCEQDLKEIERCIKVFLHENGEEGSLASVIIISA	2767
Db	1981	RYAADINSRLIRQVERLKQEAVTVPVCEQDLKEIERCIKVFLHENGEEGSLASVIIISA	2040
Qy	2768	LCTLTRRNLMMEGAASSAGEQLVDLTSRDGAWFLEELCSMSGNVTCVLQLLKQCHLVPQD	2827
Db	2041	LCTLTRRNLMMEGAASSAGEQLVDLTSRDGAWFLEELCSMSGNVTCVLQLLKQCHLVPQD	2100
Qy	2828	LDIPNPMEASETVHLANGVYTSLQELNSNFRQIIFPEALRCLMKGEYTTLESMLHELDGLI	2887
Db	2101	LDIPNPMEASETVHLANGVYTSLQELNSNFRQIIFPEALRCLMKGEYTTLESMLHELDGLI	2160
Qy	2888	EQTTDGVPLQTLVESLQAYLRNAAMGLEEETHAHYIDVARLLHAQYGELIQPRNGSVDET	2947
Db	2161	EQTTDGVPLQTLVESLQAYLRNAAMGLEEETHAHYIDVARLLHAQYGELIQPRNGSVDET	2220
Qy	2948	PKMSAGQMLLVAFDGMFAQVETAFSLLEKLNKMEIPIAWRKIDIIREARSTQVNFDDDD	3007
Db	2221	PKMSAGQMLLVAFDGMFAQVETAFSLLEKLNKMEIPIAWRKIDIIREARSTQVNFDDDD	2280
Qy	3008	NHRQVLEEIFFLKRLQTIKEFFRLCGTFSKTLGSSSSLEDQNTVNGPVQIVNVKTLFRNS	3067
Db	2281	NHRQVLEEIFFLKRLQTIKEFFRLCGTFSKTLGSSSSLEDQNTVNGPVQIVNVKTLFRNS	2340
Qy	3068	CFSEDQMAKPIKAFTADFVRQLLIGLPNQAALGLTLCFSFISALGVDIIAQVEAKDFGAESK	3127
Db	2341	CFSEDQMAKPIKAFTADFVRQLLIGLPNQAALGLTLCFSFISALGVDIIAQVEAKDFGAESK	2400
Qy	3128	VSVDLCKKAVEHNIQIGKFSQLVMNRATVLASSYDTAWKKHDLVRRLETSISSCKTSLQ	3187
Db	2401	VSVDLCKKAVEHNIQIGKFSQLVMNRATVLASSYDTAWKKHDLVRRLETSISSCKTSLQ	2460
Qy	3188	RVQLHIAMFQWQHEDLLINRPQAMSVTPPPRSAILTSMKKKLHTLSQIETSIATVQEKLA	3247
Db	2461	RVQLHIAMFQWQHEDLLINRPQAMSVTPPPRSAILTSMKKKLHTLSQIETSIATVQEKLA	2520
Qy	3248	ALESSIEQRLKWAGGANPALAPVLQDFEATIAERRNLVLKESQRASQVTFLCSNIIHFES	3307
Db	2521	ALESSIEQRLKWAGGANPALAPVLQDFEATIAERRNLVLKESQRASQVTFLCSNIIHFES	2580
Qy	3308	LRTRTAEALNLDAALELIKRCQQMCFSASFQFNSSVSELELRLLQRVDTGLEHPISSEW	3367
Db	2581	LRTRTAEALNLDAALELIKRCQQMCFSASFQFNSSVSELELRLLQRVDTGLEHPISSEW	2640
Qy	3368	LLSAHKQLTQDMSTQRAIQTEKEQQIETVCETIQNLVDNIKTVLTGHNRLQGDVKHLLKA	3427
Db	2641	LLSAHKQLTQDMSTQRAIQTEKEQQIETVCETIQNLVDNIKTVLTGHNRLQGDVKHLLKA	2700



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